



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/500,796
Source: PET
Date Processed by STIC: 7/13/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM; ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04



PCT

RAW SEQUENCE LISTING

DATE: 07/13/2004

PATENT APPLICATION: US/10/500,796

TIME: 16:36:17

Input Set : A:\64909-02 SEQ LIST.TXT

Output Set: N:\CRF4\07132004\J500796.raw

4 <110> APPLICANT: The Government of the United States of America, as represented by the
 5 Secretary, Department of Health and Human Services, c/o Centers for
 6 Disease Control and Prevention
 8 Chang, Gwong-Jen J
 10 <120> TITLE OF INVENTION: Nucleic Acid Vaccines for Prevention of
 11 Flavivirus Infection
 13 <130> FILE REFERENCE: 6395-64909-02
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/500,796
 C--> 15 <141> CURRENT FILING DATE: 2004-07-06
 15 <150> PRIOR APPLICATION NUMBER: PCT/US02/10764
 16 <151> PRIOR FILING DATE: 2002-04-04
 18 <150> PRIOR APPLICATION NUMBER: 09/826,115
 19 <151> PRIOR FILING DATE: 2001-04-04
 21 <150> PRIOR APPLICATION NUMBER: 09/701,536
 22 <151> PRIOR FILING DATE: 2000-11-29
 24 <150> PRIOR APPLICATION NUMBER: PCT/US99/12298
 25 <151> PRIOR FILING DATE: 1999-06-03
 27 <150> PRIOR APPLICATION NUMBER: 60/087,908
 28 <151> PRIOR FILING DATE: 1998-06-04
 30 <160> NUMBER OF SEQ ID NOS: 61
 32 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 34 <210> SEQ ID NO: 1
 35 <211> LENGTH: 48
 36 <212> TYPE: DNA
 37 <213> ORGANISM: Artificial Sequence
 39 <220> FEATURE:
 40 <223> OTHER INFORMATION: Description of artificial sequence; note =
 41 synthetic construct
 W--> 43 <221> NAME/KEY: CDS
 44 <222> LOCATION: (25)...(48)
 W--> 46 <221> misc_feature
 47 <222> LOCATION: 1-48
 48 <223> OTHER INFORMATION: Amplimer 14DV389
 W--> 50 <400> 1
 51 cttggtacct cttagagccgc cgcc atg ggc aga aag caa aac aaa aga 48
 52 Met Gly Arg Lys Gln Asn Lys Arg
 53 1 5
 56 <210> SEQ ID NO: 2
 57 <211> LENGTH: 8
 58 <212> TYPE: PRT
 59 <213> ORGANISM: Artificial Sequence
 61 <220> FEATURE:
 62 <223> OTHER INFORMATION: Description of artificial sequence; note =

Does Not Comply
 Corrected Diskette Needed
 (Pg.3)

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63      synthetic construct
65 <400> SEQUENCE: 2
66 Met Gly Arg Lys Gln Asn Lys Arg
67 1      5
69 <210> SEQ ID NO: 3
70 <211> LENGTH: 50
71 <212> TYPE: DNA
72 <213> ORGANISM: Artificial Sequence
74 <220> FEATURE:
75 <223> OTHER INFORMATION: Description of artificial sequence; note =
76      synthetic construct
W--> 78 <221> NAME/KEY: misc_feature
79 <222> LOCATION: 1-50
80 <223> OTHER INFORMATION: Amplimer c14DV2453
W--> 82 <400> 3
83 ttttcttttg cggccgctca aacttaagca tgcacattgg tcgctaagaa      50
85 <210> SEQ ID NO: 4
86 <211> LENGTH: 48
87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial Sequence
90 <220> FEATURE:
91 <223> OTHER INFORMATION: Description of artificial sequence; note =
92      synthetic construct
W--> 94 <221> NAME/KEY: CDS
95 <222> LOCATION: (25)...(48)
W--> 97 <221> misc_feature
98 <222> LOCATION: (1)...(48)
99 <223> OTHER INFORMATION: Amplimer YFDV389
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103      Met Arg Ser His Asp Val Leu Thr
104      1      5
107 <210> SEQ ID NO: 5
108 <211> LENGTH: 8
109 <212> TYPE: PRT
110 <213> ORGANISM: Artificial Sequence
112 <220> FEATURE:
113 <223> OTHER INFORMATION: Description of artificial sequence; note =
114      synthetic construct
116 <400> SEQUENCE: 5
117 Met Arg Ser His Asp Val Leu Thr
118 1      5
120 <210> SEQ ID NO: 6
121 <211> LENGTH: 41
122 <212> TYPE: DNA
123 <213> ORGANISM: Artificial Sequence
125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of artificial sequence; note =
127      synthetic construct

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W--> 129 <221> NAME/KEY: misc_feature
 130 <222> LOCATION: 1-41
 131 <223> OTHER INFORMATION: Amplimer cYFDV2452

W--> 133 <400> 6
 134 ttttcttttg cggccgctca cgccccaact cctagagaaa c 41
 136 <210> SEQ ID NO: 7
 137 <211> LENGTH: 51
 138 <212> TYPE: DNA
 139 <213> ORGANISM: Artificial Sequence
 141 <220> FEATURE:
 142 <223> OTHER INFORMATION: Description of artificial sequence; note =
 143 synthetic construct

W--> 145 <221> NAME/KEY: CDS
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 W--> 148 <221> misc_feature
 W--> 149 <222> LOCATION: 1-54
 150 <223> OTHER INFORMATION: Amplimer SLEDV410

W--> 152 <400> 7
 153 cttggtacct ctagagccgc cgcc atg tct aaa aaa aga gga ggg acc aga 51
 154 Met Ser Lys Lys Arg Gly Gly Thr Arg
 155 1 5
 158 <210> SEQ ID NO: 8
 159 <211> LENGTH: 9
 160 <212> TYPE: PRT
 161 <213> ORGANISM: Artificial Sequence
 163 <220> FEATURE:
 164 <223> OTHER INFORMATION: Description of artificial sequence; note =
 165 synthetic construct
 167 <400> SEQUENCE: 8
 168 Met Ser Lys Lys Arg Gly Gly Thr Arg
 169 1 5
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 172 <211> LENGTH: 38
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 174 <213> ORGANISM: Artificial Sequence
 176 <220> FEATURE:
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 178 synthetic construct

W--> 180 <221> NAME/KEY: misc_feature
 181 <222> LOCATION: 1-38
 182 <223> OTHER INFORMATION: Amplimer cSLEDV2449

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 185 ttttcttttg cggccgctta ggcttgacg ctggttgc 38
 187 <210> SEQ ID NO: 10
 188 <211> LENGTH: 7500
 189 <212> TYPE: DNA
 190 <213> ORGANISM: Artificial Sequence
 192 <220> FEATURE:
 193 <223> OTHER INFORMATION: Description of artificial sequence; note =

There are only 51
 Nucleotides shown per <211>
 response

The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

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197 <222> LOCATION: (916)...(3009)
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200 <222> LOCATION: 1-7500
201 <223> OTHER INFORMATION: pCDJE 2-7
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205 ccgcatagtt aagccagtat ctgctccctg cttgtgtgtt ggaggtcgct gagtagtgcg      120
206 cgagcaaaat ttaagctaca acaaggcaag gcttgaccga caattgcatg aagaatctgc      180
207 ttaggggttag gcgttttgcg ctgcttcgcg atgtacgggc cagatatacg cgttgacatt      240
208 gattattgac tagttattaa tagtaatcaa ttacgggggtc attagttcat agcccatata      300
209 tggagttccg cgttacataa cttacggtaa atggcccgcg tggctgaccg cccaacgacc      360
210 cccgcccatt gacgtcaata atgacgtatg ttcccatagt aacgcccaata gggactttcc      420
211 attgacgtca atgggtggac tatttacggg aaactgccca cttggcagta catcaagtgt      480
212 atcatatgcc aagtagcccc cctattgacg tcaatgacgg taaatggccc gcctggcatt      540
213 atgcccagta catgacctta tgggactttc ctacttgga gtacatctac gtattagtca      600
214 tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg      660
215 actcacgggg atttccaagt ctccaccca ttgacgtcaa tgggagtttg ttttggcacc      720
216 aaaatcaacg ggactttcca aaatgtcgta acaactccgc ccattgacg caaatgggcg      780
217 gtaggcgtgt acgggtgggag gtctatataa gcagagctct ctggctaact agagaaccca      840
218 ctgcttactg gcttatcgaa attaatacga ctactatag ggagacccaa gcttggtacc      900
219 gagctcgccg ccgcc atg ggc aga aag caa aac aaa aga gga gga aat gaa      951
220      Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu
221      1      5      10
223 ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg      999
224 Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala
225      15      20      25
227 gga gcc atg aag ttg tgc aat ttc cag ggg aag ctt ttg atg acc atc      1047
228 Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile
229      30      35      40
231 aac aac acg gac att gca gac gtt atc gtg att ccc acc tca aaa gga      1095
232 Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly
233      45      50      55      60
235 gag aac aga tgc tgg gtc cgg gca atc gac gtc ggc tac atg tgt gag      1143
236 Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu
237      65      70      75
239 gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca      1191
240 Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro
241      80      85      90
243 gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat      1239
244 Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr
245      95      100      105
247 gga cgg tgc acg cgg acc agg cat tcc aag cga agc agg aga tcc gtg      1287
248 Gly Arg Cys Thr Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val
249      110      115      120
251 tcg gtc caa aca cat ggg gag agt tca cta gtg aat aaa aaa gag gct      1335
252 Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala
253 125      130      135      140

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255	tgg	ctg	gat	tca	acg	aaa	gcc	aca	cga	tat	ctc	atg	aaa	act	gag	aac	1383
256	Trp	Leu	Asp	Ser	Thr	Lys	Ala	Thr	Arg	Tyr	Leu	Met	Lys	Thr	Glu	Asn	
257					145				150					155			
259	tgg	atc	ata	agg	aat	cct	ggc	tat	gct	ttc	ctg	gcg	gcg	gta	ctt	ggc	1431
260	Trp	Ile	Ile	Arg	Asn	Pro	Gly	Tyr	Ala	Phe	Leu	Ala	Ala	Val	Leu	Gly	
261					160				165					170			
263	tgg	atg	ctt	ggc	agt	aac	aac	ggg	caa	cgc	gtg	gta	ttt	acc	atc	ctc	1479
264	Trp	Met	Leu	Gly	Ser	Asn	Asn	Gly	Gln	Arg	Val	Val	Phe	Thr	Ile	Leu	
265					175				180					185			
267	ctg	ctg	ttg	gtc	gct	ccg	gct	tac	agt	ttt	aat	tgt	ctg	gga	atg	ggc	1527
268	Leu	Leu	Leu	Val	Ala	Pro	Ala	Tyr	Ser	Phe	Asn	Cys	Leu	Gly	Met	Gly	
269					190				195					200			
271	aat	cgt	gac	ttc	ata	gaa	gga	gcc	agt	gga	gcc	act	tgg	gtg	gac	ttg	1575
272	Asn	Arg	Asp	Phe	Ile	Glu	Gly	Ala	Ser	Gly	Ala	Thr	Trp	Val	Asp	Leu	
273	205					210						215				220	
275	gtg	ctg	gaa	gga	gat	agc	tgc	ttg	aca	atc	atg	gca	aac	gac	aaa	cca	1623
276	Val	Leu	Glu	Gly	Asp	Ser	Cys	Leu	Thr	Ile	Met	Ala	Asn	Asp	Lys	Pro	
277					225						230				235		
279	aca	ttg	gac	gtc	cgc	atg	att	aac	atc	gaa	gct	agc	caa	ctt	gct	gag	1671
280	Thr	Leu	Asp	Val	Arg	Met	Ile	Asn	Ile	Glu	Ala	Ser	Gln	Leu	Ala	Glu	
281					240					245					250		
283	gtc	aga	agt	tac	tgc	tat	cat	gct	tca	gtc	act	gac	atc	tcg	acg	gtg	1719
284	Val	Arg	Ser	Tyr	Cys	Tyr	His	Ala	Ser	Val	Thr	Asp	Ile	Ser	Thr	Val	
285					255				260					265			
287	gct	cgg	tgc	ccc	acg	act	gga	gaa	gcc	cac	aac	gag	aag	cga	gct	gat	1767
288	Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	Ala	His	Asn	Glu	Lys	Arg	Ala	Asp	
289					270				275					280			
291	agt	agc	tat	gtg	tgc	aaa	caa	ggc	ttc	act	gac	cgt	ggg	tgg	ggc	aac	1815
292	Ser	Ser	Tyr	Val	Cys	Lys	Gln	Gly	Phe	Thr	Asp	Arg	Gly	Trp	Gly	Asn	
293	285					290						295				300	
295	gga	tgt	gga	ctt	ttc	ggg	aag	gga	agc	att	gac	aca	tgt	gca	aaa	ttc	1863
296	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Asp	Thr	Cys	Ala	Lys	Phe	
297					305					310					315		
299	tcc	tgc	acc	agt	aaa	gcg	att	ggg	aga	aca	atc	cag	cca	gaa	aac	atc	1911
300	Ser	Cys	Thr	Ser	Lys	Ala	Ile	Gly	Arg	Thr	Ile	Gln	Pro	Glu	Asn	Ile	
301					320				325					330			
303	aaa	tac	gaa	gtt	ggc	att	ttt	gtg	cat	gga	acc	acc	act	tcg	gaa	aac	1959
304	Lys	Tyr	Glu	Val	Gly	Ile	Phe	Val	His	Gly	Thr	Thr	Thr	Ser	Glu	Asn	
305					335				340					345			
309	cat	ggg	aat	tat	tca	gcg	caa	gtt	ggg	gcg	tcc	cag	gcg	gca	aag	ttt	2007
310	His	Gly	Asn	Tyr	Ser	Ala	Gln	Val	Gly	Ala	Ser	Gln	Ala	Ala	Lys	Phe	
311					350				355					360			
313	aca	gta	aca	ccc	aat	gct	cct	tcg	ata	acc	ctc	aaa	ctt	ggg	gac	tac	2055
314	Thr	Val	Thr	Pro	Asn	Ala	Pro	Ser	Ile	Thr	Leu	Lys	Leu	Gly	Asp	Tyr	
315	365					370					375				380		
317	gga	gaa	gtc	aca	ctg	gac	tgt	gag	cca	agg	agt	gga	ctg	aac	act	gaa	2103
318	Gly	Glu	Val	Thr	Leu	Asp	Cys	Glu	Pro	Arg	Ser	Gly	Leu	Asn	Thr	Glu	
319					385					390					395		
321	gcg	ttt	tac	gtc	atg	acc	gtg	ggg	tca	aag	tca	ttt	ctg	gtc	cat	agg	2151

VERIFICATION SUMMARY

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Input Set : A:\64909-02 SEQ LIST.TXT

Output Set: N:\CRF4\07132004\J500796.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application No
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:43 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:46 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:50 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:78 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:82 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:94 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:97 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:101 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:129 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:133 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:145 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:146 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#:7, CDS LOCATION: (25)...
(54)
L:148 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
L:152 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:7
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L:184 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:9
L:196 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
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L:486 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:11
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L:591 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:12
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L:643 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:15
L:892 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:16
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L:2429 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
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Input Set : A:\64909-02 SEQ LIST.TXT

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L:2449 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:29
L:2461 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:2465 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:30
L:2477 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:2481 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:31
L:2655 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:2658 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:42
L:2996 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:2999 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:44
L:3335 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3338 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:46